Jarrell, Noble

From:

Ramirez, Delia

Sent:

Wednesday, April 19, 2006 6:24 PM

To: Subject:

Jarrell, Noble 10/665455

Hi,

I would like to request the following alignments: SEQ ID NO:1 against SEQ ID NO:2-7.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

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Results of SIM with:

Sequence 1: UserSeq1, (180 residues) Sequence 2: UserSeq2, (177 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20

Gap open penalty: 12
Gap extension penalty: 4

SER 12 NO:1 VS

SERVID NO: 2

(PROTEIN TRANSCATION)



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.9% identity in 177 residues overlap; Score: 927.0; Gap frequency: 0.0%

UserSeq1, UserSeq2,

MPIEYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLL@SSAMASFRREMVNTLGIER

MPIK*KPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLØF\$AMASFRREMVNTLGIER ***********

4

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UserSeq2,
                   UserSeq1,
                                                                                                                                                                                        UserSeq1,
                                                                                                                                                                                                                                                                                                                                      UserSeq2
                                                                      26.7% identity in
                                                                                                                                                                 UserSeq2,
                                                                                                                                                                                                                                                                                                                                                            UserSeq1,
                                                                                                                                                                                                                                                                                                                                                                                                              57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
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                                                                                                                                                                                                                                         identity in
                                                                                                                                                                                                                                                                                                                                          136
                       154 GYACAYSSAFMGREI
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GYQSGLKDAELARKL
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                                                                   residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                      residues overlap; Score: 21.0; Gap frequency: 0.0%
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You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 2: UserSeq2, (180 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

SED ID 10:1 US. SERID NO:3



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

UserSeq1, 98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

UserSeq2, MP İKYKPE I QHSDFKDLTNLI HFQSMEGKI WLGEQRMLLLQFSAMASFRREMVNTLGI ER MP TEYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQ\$\$AMASFRREMVNTLGIER *************************

ja,

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UserSeq2,
                   UserSeq1,
                                                                                                                                                                  UserSeq2,
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                                                                       33.3% identity in
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                                                                                                                                                                                                                                            26.7% identity in
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  107 KVRPTGLDI
                                                                                                                                                                    154 GYACAYSSAFMGREI
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                                                                      residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                           residues overlap; Score: 21.0; Gap frequency: 0.0%
```

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Results of SIM with:

Sequence 1: UserSeq1, (180 residues) Sequence 2: UserSeq2, (180 residues)

SEN ID NO: 1 VS SEDIDNO: 4

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.8% identity in 180 residues overlap; Score: 938.0; Gap frequency: 0.0%

 μ MP JKYKPE JRHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQFSAMASFRREMVNTLGIER MP1/EKKPEI/QHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQSSAMASFRREMVNTLGIER 0

UserSeq1, UserSeq2,

A CONTRACT NOON

```
UserSeq2,
                                              UserSeq1,
                                                                                                                                UserSeq2,
                                                                                                                                                          UserSeq1,
                        121
                                                 121
                                                                                                                                   61
                     RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGCGG
                                              RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGCGG
                                                                                                                              AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDMEYG
                                                                                                                                                       AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDI ÜKEYG
*******************
                                                                                                         ******************
                                                                                                                                                                                                      三
```

UserSeq1, UserSeq2, 36.4% identity in 107 KVRPTELDIDM KLRPNASEVGM 11 residues overlap; Score: 24.0; Gap frequency: 0.0%

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * * * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * * **

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL
UserSeq2, 154 GYACAYSSAFMGREI

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Results of SIM with:

Sequence 2: UserSeq2, (180 residues) Sequence 1: UserSeq1, (180 residues)

using the parameters

SECO IDIN: INS SECO ID NO: 5

Comparison matrix: BLOSUM62

Number of alignments computed: 20 Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 936.0; Gap frequency: 0.0%

UserSeq2, UserSeq1,

MP ΙΈΥΚΡΕΙ QHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLØSÅAMASFRREMVNTLGÆR

بر بر MP ¶K¥KPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLФF\$AMASFRREMVNTLGVER ******************* *************

22

```
UserSeq1,
UserSeq2,
UserSeq2,
                    UserSeq1,
                                                                 26.7% identity in
                                                                                                                                                                       UserSeq1,
                                                                                                                                                                                                                                                                                                      UserSeq2,
                                                                                                                                                                                                                                                                                                                          UserSeq1,
                                                                                                                                                 UserSeq2,
                                                                                                                                                                                                                    26.7%
                                                                                                                                                                                                                                                                                                                                                                     57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                          UserSeq2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UserSeq1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UserSeq2,
                                                                                                                                                                                                                    identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                      154 GYACAYSSAFMGREI
                                                                                                                                                   154 GYACAYSSAFMGREI
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 69 GYQSGLKDAELARKL
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                                                                                                                                                                         GYQSGLKDAELARKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCWTVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICQTDLG
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                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * * **
                                                             residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                                   residues overlap;
                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *****************
                                                                                                                                                                                                                   21.0;
                                                                                                                                                                                                                 Gap frequency: 0.0%
```

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Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

using the parameters

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

SEO DUIVS SEIDNES



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 932.0; Gap frequency: 0.0%

UserSeq2, UserSeq1,

MPI/EYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQS\\ AMASFRREMVNTLGIER

MP¶KŸKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLØF\$AMASFRREMVNTLGIER ************* ***********

```
40.0% identity in
                                                                                                              UserSeq2,
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                                                                                                                                                                                                                                                            UserSeq1,
                                                                                                                                            121
                                                                                                             121 RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSALMGREIIFKEVSCRGCGG
                                                                                                                                                                                                                                                          61
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                                                                                                                                          RFYAEMEWIDWFEVEICQTDLGQMQDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGCGG
                                                                                                                                                                                                                                AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIGREYG
                                                                                                                                                                                                                                                          AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDI|DK|EYG
                                                                                       *******************
                                                                                                                                                                                                          ******************
10 residues overlap; Score: 26.0; Gap frequency: 0.0%
                                                                                                                                                                                                                                                                                                                       111-011
```

UserSeq1, UserSeq2, 107 82 KVRPTELDIG KLRPNASEVG

UserSeq2, UserSeq1, 57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0% 136 ICQTDLG 148 VCWTVLG

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL



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Results of SIM with:

Sequence 1: UserSeq1, (180 residues) Sequence 2: UserSeq2, (180 residues)

JER 15 20:1 VS SER 12 20:7

using the parameters.

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

UserSeq2, UserSeq1, ΜΡ ΓΙΈΥ KPEI QHSDFKDLTNLIHFQSMEGKIWLGEQRMLLL Θ΄SSAMASFRREMVNTLGIER MP¶KYKPEIQHSDFKDLTNLIHFQSMEGKIWLGEQRMLLLQF\$AMASFRREMVNTLGIER *** 4 ************



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UserSeq1,
UserSeq2,
UserSeq2,
                   UserSeq1,
                                                                                                                                               UserSeq2,
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                                                               33.3% identity in
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                                                                                                                                                                                                             identity in
                      107 KVRPTELDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                148
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                                                             9 residues overlap; Score:
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                                                                                                                                                                                                                                                                                                                                                           residues overlap; Score: 21.0; Gap frequency: 0.0%
                                                                                                                                                                                                             residues overlap;
                                                                                                                                                                                                             Score: 21.0; Gap frequency: 0.0%
                                                           20.0; Gap frequency: 0.0%
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